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**RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/902,516**DATE: 11/25/98  
TIME: 18:41:18**INPUT SET: S29984.raw**

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

1                   **SEQUENCE LISTING**  
2  
3     (1)    General Information:  
4  
5        (i) APPLICANT: Soo Hoo, William  
6  
7        (ii) TITLE OF INVENTION: MEMBRANE-BOUNDED CYTOKINE COMPOSITIONS  
8                    COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE  
9                    RESPONSE USING SAME  
10  
11      (iii) NUMBER OF SEQUENCES: 50  
12  
13      (iv) CORRESPONDENCE ADDRESS:  
14        (A) ADDRESSEE: CAMPBELL & FLORES, LLP  
15        (B) STREET: 4370 La Jolla Village Drive, Suite 700  
16        (C) CITY: San Diego  
17        (D) STATE: California  
18        (E) COUNTRY: United States  
19        (F) ZIP: 92121  
20  
21      (v) COMPUTER READABLE FORM:  
22        (A) MEDIUM TYPE: Floppy disk  
23        (B) COMPUTER: IBM PC compatible  
24        (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
25        (D) SOFTWARE: PatentIn Release #1.0, Version #1.25  
26  
27      (vi) CURRENT APPLICATION DATA:  
28        (A) APPLICATION NUMBER: US 08/902,516  
29        (B) FILING DATE: 29-JUL-1997  
30        (C) CLASSIFICATION:  
31  
32      (viii) ATTORNEY/AGENT INFORMATION:  
33        (A) NAME: Campbell, Cathryn A.  
34        (B) REGISTRATION NUMBER: 31,815  
35        (C) REFERENCE/DOCKET NUMBER: P-IM 2442  
36  
37      (ix) TELECOMMUNICATION INFORMATION:  
38        (A) TELEPHONE: (619)535-9001  
39        (B) TELEFAX: (619)535-8949  
40  
41  
42     (2) INFORMATION FOR SEQ ID NO:1:  
43  
44        (i) SEQUENCE CHARACTERISTICS:  
45        (A) LENGTH: 660 base pairs  
46        (B) TYPE: nucleic acid**ENTERED**

**RAW SEQUENCE LISTING  
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47                   (C) STRANDEDNESS: both  
48                   (D) TOPOLOGY: linear

49

50

51                   (ix) FEATURE:

52                   (A) NAME/KEY: CDS  
53                   (B) LOCATION: 1..660

54

55

56                   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

57

58       ATG GAG ACA GAC ACA CTC CTG CTA TGG GTA CTG CTG CTC TGG GTT CCA	48
59       Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro	
60       1                   5                   10                   15	

61

62       GGT TCC ACT GGG GAC TAT CCA TAT GAT GTT CCA GAT TAT GCT GGG GCC	96
63       Gly Ser Thr Gly Asp Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Ala	
64       20                   25                   30	

65

66       CAA GCA CCC ACC CGC TCA CCC ATC ACT GTC ACC CGG CCT TGG AAG CAT	144
67       Gln Ala Pro Thr Arg Ser Pro Ile Thr Val Thr Arg Pro Trp Lys His	
68       35                   40                   45	

69

70       GTA GAG GCC ATC AAA GAA GCC CTG AAC CTC CTG GAT GAC ATG CCT GTC	192
71       Val Glu Ala Ile Lys Glu Ala Leu Asn Leu Leu Asp Asp Met Pro Val	
72       50                   55                   60	

73

74       ACG TTG AAT GAA GAG GTA GAA GTC GTC TCT AAC GAG TTC TCC TTC AAG	240
75       Thr Leu Asn Glu Glu Val Val Val Ser Asn Glu Phe Ser Phe Lys	
76       65                   70                   75                   80	

77

78       AAG CTA ACA TGT GTG CAG ACC CGC CTG AAG ATA TTC GAG CAG GGT CTA	288
79       Lys Leu Thr Cys Val Gln Thr Arg Leu Lys Ile Phe Glu Gln Gly Leu	
80       85                   90                   95	

81

82       CGG GGC AAT TTC ACC AAA CTC AAG GGC GCC TTG AAC ATG ACA GCC AGC	336
83       Arg Gly Asn Phe Thr Lys Leu Lys Gly Ala Leu Asn Met Thr Ala Ser	
84       100                   105                   110	

85

86       TAC TAC CAG ACA TAC TGC CCC CCA ACT CCG GAA ACG GAC TGT GAA ACA	384
87       Tyr Tyr Gln Thr Tyr Cys Pro Pro Thr Pro Glu Thr Asp Cys Glu Thr	
88       115                   120                   125	

89

90       CAA GTT ACC ACC TAT GCG GAT TTC ATA GAC AGC CTT AAA ACC TTT CTG	432
91       Gln Val Thr Thr Tyr Ala Asp Phe Ile Asp Ser Leu Lys Thr Phe Leu	
92       130                   135                   140	

93

94       ACT GAT ATC CCC TTT GAA TGC AAA AAA CCA GGC CAA AAA GTC GAC GAA	480
95       Thr Asp Ile Pro Phe Glu Cys Lys Lys Pro Gly Gln Lys Val Asp Glu	
96       145                   150                   155                   160	

97

98       CAA AAA CTC ATC TCA GAA GAG GAT CTG AAT GCT GTG GGC CAG GAC ACG	528
99       Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ala Val Gly Gln Asp Thr	

## INPUT SET: S29984.raw

100                   165                   170                   175  
101  
102 CAG GAG GTC ATC GTG GTG CCA CAC TCC TTG CCC TTT AAG GTG GTG GTG       576  
103 Gln Glu Val Ile Val Val Pro His Ser Leu Pro Phe Lys Val Val Val  
104                   180                   185                   190  
105  
106 ATC TCA GCC ATC CTG GCC CTG GTG GTG CTC ACC ATC ATC TCC CTT ATC       624  
107 Ile Ser Ala Ile Leu Ala Leu Val Val Leu Thr Ile Ile Ser Leu Ile  
108                   195                   200                   205  
109  
110 ATC CTC ATC ATG CTT TGG CAG AAG AAG CCA CGT TAG                   660  
111 Ile Leu Ile Met Leu Trp Gln Lys Lys Pro Arg  
112                   210                   215                   220  
113  
114  
115 (2) INFORMATION FOR SEQ ID NO:2:  
116  
117                   (i) SEQUENCE CHARACTERISTICS:  
118                   (A) LENGTH: 219 amino acids  
119                   (B) TYPE: amino acid  
120                   (D) TOPOLOGY: linear  
121  
122                   (ii) MOLECULE TYPE: protein  
123  
124                   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
125  
126 Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro     80  
127       1           5                   10                   15  
128  
129 Gly Ser Thr Gly Asp Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Ala     160  
130       20           25                   30  
131  
132 Gln Ala Pro Thr Arg Ser Pro Ile Thr Val Thr Arg Pro Trp Lys His     240  
133       35           40                   45  
134  
135 Val Glu Ala Ile Lys Glu Ala Leu Asn Leu Leu Asp Asp Met Pro Val     280  
136       50           55                   60  
137  
138 Thr Leu Asn Glu Glu Val Glu Val Val Ser Asn Glu Phe Ser Phe Lys     320  
139       65           70                   75                   80  
140  
141 Lys Leu Thr Cys Val Gln Thr Arg Leu Lys Ile Phe Glu Gln Gly Leu     360  
142       85           90                   95  
143  
144 Arg Gly Asn Phe Thr Lys Leu Lys Gly Ala Leu Asn Met Thr Ala Ser     400  
145       100           105                   110  
146  
147 Tyr Tyr Gln Thr Tyr Cys Pro Pro Thr Pro Glu Thr Asp Cys Glu Thr     440  
148       115           120                   125  
149  
150 Gln Val Thr Thr Tyr Ala Asp Phe Ile Asp Ser Leu Lys Thr Phe Leu     480  
151       130           135                   140  
152

RAW SEQUENCE LISTING  
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153 Thr Asp Ile Pro Phe Glu Cys Lys Lys Pro Gly Gln Lys Val Asp Glu  
154 145 150 155 160  
155  
156 Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ala Val Gly Gln Asp Thr  
157 165 170 175  
158  
159 Gln Glu Val Ile Val Val Pro His Ser Leu Pro Phe Lys Val Val Val  
160 180 185 190  
161  
162 Ile Ser Ala Ile Leu Ala Leu Val Val Leu Thr Ile Ile Ser Leu Ile  
163 195 200 205  
164  
165 Ile Leu Ile Met Leu Trp Gln Lys Lys Pro Arg  
166 210 215  
167  
168  
169 (2) INFORMATION FOR SEQ ID NO:3:  
170  
171 (i) SEQUENCE CHARACTERISTICS:  
172 (A) LENGTH: 9 amino acids  
173 (B) TYPE: amino acid  
174 (D) TOPOLOGY: linear  
175  
176 (ii) MOLECULE TYPE: peptide  
177  
178  
179  
180 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:  
181  
182 Val Gln Gly Glu Glu Ser Asn Asp Lys  
183 1 5  
184  
185 (2) INFORMATION FOR SEQ ID NO:4:  
186  
187 (i) SEQUENCE CHARACTERISTICS:  
188 (A) LENGTH: 25 amino acids  
189 (B) TYPE: amino acid  
190 (D) TOPOLOGY: linear  
191  
192 (ii) MOLECULE TYPE: peptide  
193  
194  
195  
196 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:  
197  
198 Phe Ile Leu Pro Ile Leu Gly Ala Val Leu Ala Leu Leu Leu Leu  
199 1 5 10 15  
200  
201 Thr Leu Leu Ala Leu Leu Leu Val  
202 20 25  
203  
204 (2) INFORMATION FOR SEQ ID NO:5:  
205

**RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/902,516**

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## **INPUT SET: S29984.raw**

206 (i) SEQUENCE CHARACTERISTICS:  
207 (A) LENGTH: 26 amino acids  
208 (B) TYPE: amino acid  
209 (D) TOPOLOGY: linear  
210  
211 (ii) MOLECULE TYPE: peptide  
212  
213  
214  
215 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:  
216  
217 Ile Tyr Leu Ile Ile Gly Ile Cys Gly Gly Ser Leu Leu Met Val  
218 1 5 10 15  
219  
220 Phe Val Ala Leu Leu Val Phe Tyr Ile Thr  
221 20 25  
222  
223 (2) INFORMATION FOR SEQ ID NO:6:  
224  
225 (i) SEQUENCE CHARACTERISTICS:  
226 (A) LENGTH: 22 amino acids  
227 (B) TYPE: amino acid  
228 (D) TOPOLOGY: linear  
229  
230 (ii) MOLECULE TYPE: peptide  
231  
232  
233  
234 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:  
235  
236 Ala Leu Val Val Ile Pro Ile Ile Phe Gly Ile Leu Phe Ala Ile Leu  
237 1 5 10 15  
238  
239 Leu Val Leu Val Phe Ile  
240 20  
241  
242 (2) INFORMATION FOR SEQ ID NO:7:  
243  
244 (i) SEQUENCE CHARACTERISTICS:  
245 (A) LENGTH: 20 amino acids  
246 (B) TYPE: amino acid  
247 (D) TOPOLOGY: linear  
248  
249 (ii) MOLECULE TYPE: peptide  
250  
251  
252  
253 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:  
254  
255 Ile Ser Gly Ala Thr Ala Gly Val Pro Thr Leu Leu Leu Gly Leu Val  
256 1 5 10 15  
257  
258 Leu Pro Ala Pro

INPUT SET: S29984.raw

## \*\*\*\*\* PREVIOUSLY ERRORED SEQUENCES - EDITED \*\*\*\*\*

42 (2) INFORMATION FOR SEQ ID NO:1:

43

44 (i) SEQUENCE CHARACTERISTICS:  
45 (A) LENGTH: 660 base pairs  
46 (B) TYPE: nucleic acid  
47 (C) STRANDEDNESS: both  
48 (D) TOPOLOGY: linear

49

50

51 (ix) FEATURE:

52 (A) NAME/KEY: CDS  
53 (B) LOCATION: 1..660

54

55

56 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

57

58 ATG GAG ACA GAC ACA CTC CTG CTA TGG GTA CTG CTG CTC TGG GTT CCA	48
59 Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro	
60 1 5 10 15	
61 GGT TCC ACT GGG GAC TAT CCA TAT GAT GTT CCA GAT TAT GCT GGG GCC	96
62 Gly Ser Thr Gly Asp Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Ala	
63 20 25 30	
64 CAA GCA CCC ACC CGC TCA CCC ATC ACT GTC ACC CGG CCT TGG AAG CAT	144
65 Gln Ala Pro Thr Arg Ser Pro Ile Thr Val Thr Arg Pro Trp Lys His	
66 35 40 45	
67 GTA GAG GCC ATC AAA GAA GCC CTG AAC CTC CTG GAT GAC ATG CCT GTC	192
68 Val Glu Ala Ile Lys Glu Ala Leu Asn Leu Leu Asp Asp Met Pro Val	
69 50 55 60	
70 ACG TTG AAT GAA GAG GTA GAA GTC GTC TCT AAC GAG TTC TCC TTC AAG	240
71 Thr Leu Asn Glu Glu Val Val Ser Asn Glu Phe Ser Phe Lys	
72 65 70 75 80	
73 AAG CTA ACA TGT GTG CAG ACC CGC CTG AAG ATA TTC GAG CAG GGT CTA	288
74 Lys Leu Thr Cys Val Gln Thr Arg Leu Lys Ile Phe Glu Gln Gly Leu	
75 85 90 95	
76 CCG GGC AAT TTC ACC AAA CTC AAG GGC GCC TTG AAC ATG ACA GCC AGC	336
77 Arg Gly Asn Phe Thr Lys Leu Lys Gly Ala Leu Asn Met Thr Ala Ser	
78 100 105 110	
79 TAC TAC CAG ACA TAC TGC CCC CCA ACT CCG GAA ACG GAC TGT GAA ACA	384
80 Tyr Tyr Gln Thr Tyr Cys Pro Pro Thr Pro Glu Thr Asp Cys Glu Thr	
81 115 120 125	

**RAW SEQUENCE LISTING  
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89  
90 CAA GTT ACC ACC TAT GCG GAT TTC ATA GAC AGC CTT AAA ACC TTT CTG 432  
91 Gln Val Thr Thr Tyr Ala Asp Phe Ile Asp Ser Leu Lys Thr Phe Leu  
92 130 135 140  
93  
94 ACT GAT ATC CCC TTT GAA TGC AAA AAA CCA GGC CAA AAA GTC GAC GAA 480  
95 Thr Asp Ile Pro Phe Glu Cys Lys Lys Pro Gly Gln Lys Val Asp Glu  
96 145 150 155 160  
97  
98 CAA AAA CTC ATC TCA GAA GAG GAT CTG AAT GCT GTG GGC CAG GAC ACG 528  
99 Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ala Val Gly Gln Asp Thr  
100 165 170 175  
101  
102 CAG GAG GTC ATC GTG GTG CCA CAC TCC TTG CCC TTT AAG GTG GTG GTG 576  
103 Gln Glu Val Ile Val Val Pro His Ser Leu Pro Phe Lys Val Val Val  
104 180 185 190  
105  
106 ATC TCA GCC ATC CTG GCC CTG GTG GTG CTC ACC ATC ATC TCC CTT ATC 624  
107 Ile Ser Ala Ile Leu Ala Leu Val Val Val Leu Thr Ile Ile Ser Leu Ile  
108 195 200 205  
109  
110 ATC CTC ATC ATG CTT TGG CAG AAG AAG CCA CGT TAG 660  
111 Ile Leu Ile Met Leu Trp Gln Lys Lys Pro Arg  
112 210 215 220  
113  
114

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**SEQUENCE VERIFICATION REPORT**  
PATENT APPLICATION **US/08/902,516**

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Line	Error	Original Text
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